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```
CGCGTCCGGCAGATTACAGTCGTTTCCAGCCCAAGTGACCTGATCGATGGCCCTCCTGAATTTATCACGATATTTGAT
TTATTAGCGATGCCCCCTGGTTTGTGTGTACGCACACACACGTGCACACAAGGCTCTGGCTCGCTTCCCTCCCTCGTT
TCCAGCTCCTGGCGAATCCACATCTGTTTCAACTCTCCGCCGAGGCGAGCAGAGTGTCGAAATCTGCG
AGTGAAGAGGACGAGGAAAAGAAACCAAGCCACAGACGCAACTTGAGACTCCCGCATCCCAAAAGAACACAGATC

M      G      P      P      S      L      V      L      C      L      L      S      A      T      V      F      16
AGCAAAAAAGAAG ATG GGC CCC CCG AGC CTC GTG CTG TGC TGC TTG CTG TCC GCA ACT GTG TTC      48

S      L      L      G      G      S      S      A      F      L      S      H      H      R      L      K      G      R      F      Q      36
TCC CTG CTG GGT GGA AGC TCG GCC TTC CTG CTG TCG CAC CAC CAC CGC CTG AAA GGC AGG TTT CAG      108

R      D      R      R      N      I      R      P      N      I      I      L      V      L      T      D      Q      D      V      56
AGG GAC CGC AGG AAC ATC CGC CCC AAC ATC ATC CTG GTG CTG ACG GAC GAC CAG GAT GTG      168

E      L      G      S      M      Q      V      M      N      K      T      R      R      I      M      E      Q      G      G      T      76
GAG CTG GGT TCC ATG CAG GTG ATG AAC AAC AAG ACC CGG CGC ATC ATG GAG CAG GGC GGC ACG      228

H      F      I      N      A      F      V      T      P      M      C      C      C      P      S      R      S      S      I      L      96
CAC TTC ATC AAC GCC TTC GTG ACC ACA CCC ATG TGC TGC TGC CCC TCA CGC TCC TCC ATC CTC      288

T      G      K      Y      V      H      N      H      N      T      Y      T      N      E      N      C      S      S      P      116
ACC GGC AAG TAC GTC CAC AAC CAC AAC ACC TAC ACC AAC AAT GAG AAC TGC TCC TCG CCC      348

S      W      Q      A      Q      H      E      S      R      T      F      A      V      Y      L      N      S      T      G      Y      136
TCC TGG CAG GCA CAG CAG AGC CGC ACC TTT GCC GTG TAC CTC AAT AGC ACT GGC TAC      408
```

Fig. 1A

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R   T   A   F   F   G   K   Y   L   N   E   Y   N   G   S   Y   V   P   P   G   156
CGG ACA GCT TTC TTC GGG AAG TAT CTT AAT GAA TAC AAC GGC TCC TAC GTG CCA CCC GGC 468

W   K   E   W   G   V   G   L   L   K   N   S   R   F   Y   N   Y   T   L   C   R   176
TGG AAG GAG TGG GTC GGA CTC CTT AAA AAC TCC CGC TTT TAT AAC TAC ACG CTG TGT CGG 528

N   G   V   K   E   K   H   G   S   D   Y   S   K   D   Y   L   T   D   L   I   196
AAC GGG GTG AAA GAG AAG CAC GGC TCC GAC TAC TCC AAG GAT TAC CTC ACA GAC CTC ATC 588

T   N   D   S   V   S   F   F   R   T   S   S   K   K   M   Y   P   H   R   P   V   216
ACC AAT GAC AGC GTG AGC TTC TTC CGC AC GAC TCC AAG AAG ATG TAC TCC CCG CAC AGG CCA GTC 648

L   M   V   I   S   H   A   A   P   H   G   G   G   G   C   C   C   C   C   G   G   A   P   Q   Y   S   236
CTC ATG GTC ATC AGC CAT GCA GCC CCC CCC CAC GGC CCT GAG GAT TCA GGC CCA CAA TAT TCA 708

R   L   F   P   N   A   S   Q   H   I   T   P   S   Y   N   Y   A   P   N   P   256
CGC CTC TTC CCA AAC GCA TCT CAG CAC CAC ATC AC GGC CCC ATG AAG CCC ATC CAC ATG GAA TTC ACC 828

D   K   H   W   I   M   R   Y   T   G   P   M   K   P   I   H   M   E   F   T   276
GAC AAA CAC TGG ATC ATG CGC TAC ACG GGC CCC ATG AAG CCC ATC CAC ATG GAA TTC ACC 828

N   M   L   Q   R   K   R   L   Q   T   L   M   S   V   D   D   S   M   E   T   296
AAC ATG CTC CAG CGG AAG CGC TTG CAG ACC CTC ATG TCG GTG GAC GAC TCC ATG GAG ACG 888

I   Y   N   M   L   V   E   T   G   E   L   D   N   T   Y   I   V   Y   T   A   316
ATT TAC AAC ATG CTG GTT GAG ACG GGC GAG CTG GAC AAC ACG TAC ATC ATC GTA TAC ACC GCC 948
```

Fig. 1B

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D H G Y H I G Q F G L V K G K S M P Y E 336
 GAC CAC GGT TAC CAC ATC GGC CAG TTT GGC CTG GTG AAA GGG AAA TCC ATG CCA TAT GAG 1008

F D I R V P F Y V R G P N V E A G C L N 356
 TTT GAC ATC AGG GTC CCG TTC TAC GTG AGG GGC CCC AAC GTG GAA GCC GGC TGT CTG AAT 1068

P H I V L N I D L A P T I L D I A G L D 376
 CCC CAC ATC GTC CTC AAC ATT GAC CTG GCC CTC ACC ATC CTG GAC ATT GCA GGC CTG GAC 1128

I P A D M D G K S I L K L L D T E R P V 396
 ATA CCT GCG GAT ATG GAC GGC AAA TCC ATC CTC AAG CTG CTG GAC ACG GAG CGG CCG GTG 1188

N R F H L K K K M R V W R D S F L V E R 416
 AAT CGG TTT CAC TTG AAA AAG AAG ATG AGG GTC TGG CGG GAC TCC TTC TTG GTG GAG AGA 1248

G K L L H K R D N D K V D A Q E N F L 436
 GGC AAG CTG CTA CAC AAG AGA GAC AAT GAC AAG GTG GAC GCC CAG GAG GAG AAC TTT CTG 1308

P K Y Q R V K D L C Q R A E Y Q T A C E 456
 CCC AAG TAC CAG CGT GTG AAG GAC CTG TGT TGT CAG CGT GCT GAG TAC CAG ACG GCG TGT GAG 1368

Q L G Q K W Q C V E D A T G K L H K 476
 CAG CTG GGA CAG AAG TGG CAG TGT GTG GAG GAC GCC ACG GGG AAG CTG AAG CTG CAT AAG 1428

C K G P M R L G G S R A L S N L V P K Y 496
 TGC AAG GGC CCC ATG CGG CTG GGC AGC AGA GCC CTC TCC AAC CTC GTG CCC AAG TAC 1488

Fig. 1C

TAC	Y	G	G	G	S	E	A	C	T	C	D	S	G	D	Y	K	L	S	L	A	516
	G	G	G	G	AGC	GAG	GCC	TGC	ACC	TGT	GAC	AGC	GGG	GAC	TAC	AAG	CTC	AGC	CTG	GCC	1548
	TAC	GGG	CAG	CAG	AGC	GAG	GCC	TGC	ACC	TGT	GAC	AGC	GGG	GAC	TAC	AAG	CTC	AGC	CTG	GCC	
GGA	G	R	R	K	K	L	F	K	K	K	Y	K	A	S	Y	V	R	S	R	S	536
	G	R	R	K	K	L	F	K	K	K	Y	K	A	S	Y	V	R	S	R	S	
	GGA	CGC	CGG	AAA	AAA	CTC	TTC	AAG	AAG	AAG	TAC	AAG	GCC	AGC	TAT	GTC	CGC	AGT	CGC	TCC	1608
ATC	I	R	S	V	A	I	E	V	D	G	R	V	Y	H	V	G	L	G	D	A	556
	I	R	S	V	A	I	E	V	D	G	R	V	Y	H	V	G	L	G	D	A	
	ATC	CGC	TCA	GTG	GCC	ATC	GAG	GTG	GAC	GGC	AGG	GTG	TAC	CAC	GTA	GGC	CTG	GGT	GAT	GCC	1668
GCC	A	Q	P	R	N	L	T	K	R	H	W	P	G	A	P	E	D	Q	D	D	576
	A	Q	P	R	N	L	T	K	R	H	W	P	G	A	P	E	D	Q	D	D	
	GCC	CAG	CCC	CGA	AAC	CTC	ACC	AAG	CGG	CAC	TGG	CCA	GGG	GCC	CCT	GAG	GAC	CAA	GAT	GAC	1728
AAG	K	D	G	G	D	F	S	G	T	G	G	L	P	D	Y	S	A	A	N	P	596
	K	D	G	G	D	F	S	G	T	G	G	L	P	D	Y	S	A	A	N	P	
	AAG	GAT	GGT	GGG	GAC	TTC	AGT	GGC	ACT	GGA	GGC	CTT	CCC	GAC	TAC	TCA	GCC	GCC	AAC	CCC	1788
ATT	I	K	V	T	H	R	C	Y	I	L	E	N	D	T	V	Q	C	D	L	D	616
	I	K	V	T	H	R	C	Y	I	L	E	N	D	T	V	Q	C	D	L	D	
	ATT	AAA	GTG	ACA	CAT	CGG	TGC	TGC	TAC	ATC	CTA	GAG	AAC	GAC	ACA	GTC	CAG	TGT	GAC	CTG	GAC
CTG	L	Y	K	S	L	Q	A	W	K	D	H	K	L	H	I	D	H	E	I	E	636
	L	Y	K	S	L	Q	A	W	K	D	H	K	L	H	I	D	H	E	I	E	
	CTG	TAC	AAG	TCC	CTG	CAG	GCC	TGG	AAA	GAC	CAC	AAG	CTG	CAC	ATC	GAC	CAC	GAG	ATT	GAA	1908
ACC	T	L	Q	N	K	I	K	N	L	R	E	V	R	G	H	L	K	K	K	R	656
	T	L	Q	N	K	I	K	N	L	R	E	V	R	G	H	L	K	K	K	R	
	ACC	CTG	CAG	AAC	AAA	ATT	AAG	AAC	CTG	AGG	GAA	GTC	CGA	GGT	CAC	CTG	AAG	AAA	AAG	CGG	1968
CCA	P	E	E	C	D	C	H	K	I	S	Y	H	T	Q	H	K	G	R	L	K	676
	P	E	E	C	D	C	H	K	I	S	Y	H	T	Q	H	K	G	R	L	K	
	CCA	GAA	GAA	TGT	GAC	TGT	CAC	AAA	ATC	AGC	TAC	CAC	ACC	CAG	CAC	AAA	GGC	CGC	CTC	AAG	2028

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H	R	G	S	S	L	H	P	F	R	K	G	L	Q	E	K	D	K	V	W	696
CAC	AGA	GGC	TCC	AGT	CTG	CAT	CCT	TTC	AGG	AAG	GGC	CTG	CAA	GAG	AAG	GAC	AAG	GTG	TGG	2088
L	L	R	E	Q	K	R	K	K	K	L	R	K	L	L	K	R	L	Q	N	716
CTG	TTG	CGG	GAG	CAG	AAG	CGC	AAG	AAG	AAA	CTC	CGC	AAG	CTG	CTC	AAG	CGC	CTG	CAG	AAC	2148
N	D	T	C	S	M	P	G	L	T	C	F	T	H	D	N	Q	H	W	Q	736
AAC	GAC	ACG	TGC	AGC	ATG	CCA	GGC	CTC	ACG	TGC	TTC	ACC	CAC	GAC	AAC	CAG	CAC	TGG	CAG	2208
T	A	P	F	W	T	L	G	P	F	C	A	C	T	S	A	N	N	N	T	756
ACG	GCG	CCT	TTC	TGG	ACA	CTG	GGG	CCT	TTC	TGT	GCC	TGC	ACC	GAC	AGC	AAC	AAT	AAC	ACG	2268
Y	W	C	M	R	T	I	N	E	T	H	N	F	L	F	C	E	F	A	T	776
TAC	TGG	TGC	ATG	AGG	ACC	ATC	AAT	GAG	ACT	CAC	AAT	TTC	CTC	TTC	TGT	GAA	TTT	GCA	ACT	2328
G	F	L	E	Y	F	D	L	N	T	D	P	Y	Q	L	M	N	A	V	N	796
GGC	TTC	CTA	GAG	TAC	TTT	GAT	CTC	AAC	ACA	GAC	CCC	TAC	CAG	CTG	ATG	AAT	GCA	GTG	AAC	2388
T	L	D	R	D	V	L	N	Q	L	H	V	Q	L	M	E	L	R	S	C	816
ACA	CTG	GAC	AGG	GAT	GTC	CTC	AAC	CAG	CTA	CAC	GTA	CAG	CTC	ATG	GAG	CTG	AGG	AGC	TGC	2448
K	G	Y	K	Q	C	N	P	R	T	R	N	M	D	L	G	L	K	D	G	836
AAG	GGT	TAC	AAG	CAG	TGT	AAC	CCC	CGG	ACT	CGA	AAC	ATG	GAC	CTG	GGA	CTT	AAA	GAT	GGA	2508
G	S	Y	E	Q	Y	R	Q	F	Q	R	R	K	W	P	E	M	K	R	P	856
GGA	AGC	TAT	GAG	CAA	TAC	AGG	CAG	TTT	CAG	CGT	CGA	AAG	TGG	CCA	GAA	ATG	AAG	AGA	CCT	2568

Fig. 1E

870
2613

S S K S L G Q L W E G *
TCT TCC AAA TCA CTG GGA CAA CTG TGG GAA GGC TGG GAA GGT TAA
GAAACAACAGAGGTGGACCTCCAAAAACATAGAGGCATCACCTGACTGCACAGGCAATGAAAAACCATGTGGGTGATTT
CCAGCAGACCTGTGCTATTGGCCAGGAGGCCCTGAGAAAGCAAGCACGCACTCTCAGTCAACATGACAGATTCTGGAGGA
TAACCAGCAGGAGCAGAGATAACTTCAGGAAGTCCATTTTGGCCCCCTGCTTTTGGATTATACCTCACCCAGCTGC
ACAAAATGCATTTTTCGTATCAAAAAGTCAACCACTAACCCCTCCCCAGAAAGCTCACAAAGGAAAAACGGAGAGAGCCGAG
CGAGAGAGATTTCCTTGGAATTTCTCCCAAGGCGAAAGTCATTGGAATTTTAAATCATAGGGGAAAAGCAGTCCTG
TTC TAAATCCTCTTATCTTTTGTTTGTCAAAAGAAAGAACTAAAGAACGACAGAGGCAACGTGGAGAGGCTGAA
AACAGTGCAGAGACGTTTGACAAATGAGTCAGTAGCACAAAAGAGATGACATTTACCTAGCACTATAAACCCCTGGTTGCC
TCTGAAGAAACTGCCTT

Fig. 1F

FIG. 2

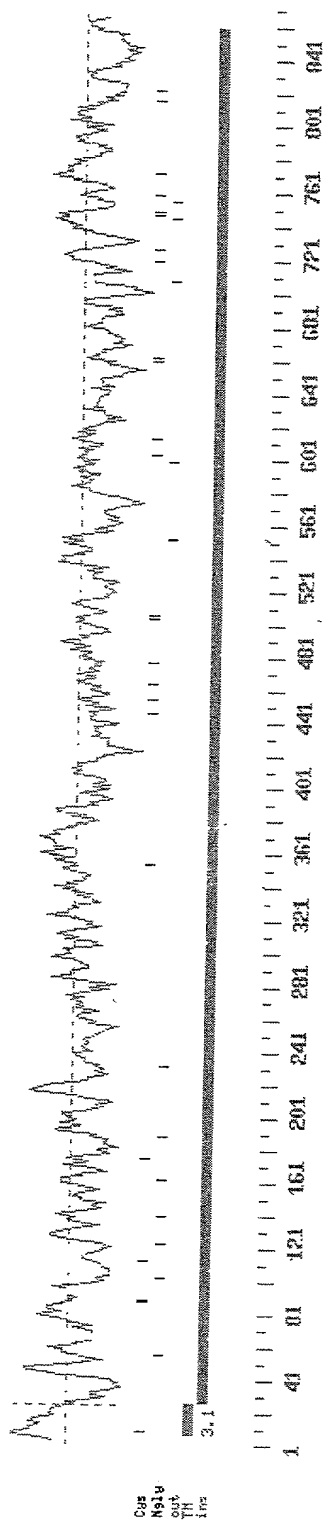


Fig. 2

Sequence Alignment

```
22437 -----  
1247 GAGCGAGAGTGTGTCGAGTGAGTGTGCGTCTGTGTGTCCCGGCGAGGGTGCGCGCTCGGC  
      10      20      30      40      50      60  
22437 -----  
1247 GCCGGGAGCGCGGCCAGCCGAGTCCGGAGGCATCGGAGGTCGAGAGCCCGGGGACCCC  
      70      80      90      100     110     120  
22437 -----  
1247 AGCTCTGCGTTCACTGCCCGGTCGCGAGCTGGACTTCGGGGCCGGGGCCGCGTGGC  
      130     140     150     160     170     180  
22437 -----  
1247 CCGGGGACAGGCAGGCGCGGTGCGCGGGCCGCGGTCCCCAGGCCGGAGATCTGCGAGT  
      190     200     210     220     230     240
```

Fig. 3A

Fig. 3B

22437	ACGGACGAC	160	170	180	190	200	210
	GATGTGGAGCTGGGTTCCATGCAGGTGATGAACAAGACCCGGCGCATC						
	ACGGACGACGAGGATGTGGAGCTGGGTTCCATGCAGGTGATGAACAAGACCCGGCGCATC						
1247	ATGGAGCAGGGGGACGCACTTCATCAACGCCTTCGTGACCACACCCCATGTGCTGCCCC						
	ATGGAGCAGGGGGACGCACTTCATCAACGCCTTCGTGACCACACCCCATGTGCTGCCCC						
1247	TCACGCTCCTCCATCCTCACCGGCAAGTACGTCCACAACCAACACACCTACACCAACAAT						
	TCACGCTCCTCCATCCTCACCGGCAAGTACGTCCACAACCAACACACCTACACCAACAAT						
22437	GAGAACTGCTCCTCGCCCTCCTGGCAGGCACACGACGAGAGCCGCACCTTTGCCCGTGTAC						
	GAGAACTGCTCCTCGCCCTCCTGGCAGGCACACGACGAGAGCCGCACCTTTGCCCGTGTAC						
1247	ATGGAGCAGGGGGACGCACTTCATCAACGCCTTCGTGACCACACCCCATGTGCTGCCCC						
	ATGGAGCAGGGGGACGCACTTCATCAACGCCTTCGTGACCACACCCCATGTGCTGCCCC						
22437	TCACGCTCCTCCATCCTCACCGGCAAGTACGTCCACAACCAACACACCTACACCAACAAT						
	TCACGCTCCTCCATCCTCACCGGCAAGTACGTCCACAACCAACACACCTACACCAACAAT						
1247	GAGAACTGCTCCTCGCCCTCCTGGCAGGCACACGACGAGAGCCGCACCTTTGCCCGTGTAC						
	GAGAACTGCTCCTCGCCCTCCTGGCAGGCACACGACGAGAGCCGCACCTTTGCCCGTGTAC						

Fig. 3C

Fig. 3D

Fig. 3E

"GAGGCTT" sequence

```
22437      880      890      900      910      920      930
GACGACTCCATGGAGACGATTACAACATGCTGGTTGAGACGGGCGAGCTGGACAACACG
1247      1210      1220      1230      1240      1250      1260
GACGACTCCATGGAGACGATTACAACATGCTGGTTGAGACGGGCGAGCTGGACAACACG
22437      940      950      960      970      980      990
TACATCGTATACACCGCCGACACCGGTTACCACATCGGCCAGTTTGGCCCTGGTGAAAGGG
1247      1270      1280      1290      1300      1310      1320
TACATCGTATACACCGCCGACACCGGTTACCACATCGGCCAGTTTGGCCCTGGTGAAAGGG
22437      1000      1010      1020      1030      1040      1050
AAATCCATGCCATATGAGTTTGACATCAGGGTCCCGTTCTACGTGAGGGGCCCCAACGTG
1247      1330      1340      1350      1360      1370      1380
AAATCCATGCCATATGAGTTTGACATCAGGGTCCCGTTCTACGTGAGGGGCCCCAACGTG
22437      1060      1070      1080      1090      1100      1110
GAAGCCGGCTGTCTGAATCCCCACATCGTCCCTCAACATTGACCTGGCCCCCACCATCCTG
1247      1390      1400      1410      1420      1430      1440
GAAGCCGGCTGTCTGAATCCCCACATCGTCCCTCAACATTGACCTGGCCCCCACCATCCTG
```

Fig. 3F

22437	GACATTGCAGGCCTGGACATAACCTGCGGATATGGACGGGAAATCCATCCTCAAGCTGCTG	1120	1130	1140	1150	1160	1170
1247	GACATTGCAGGCCTGGACATAACCTGCGGATATGGACGGGAAATCCATCCTCAAGCTGCTG	1450	1460	1470	1480	1490	1500
22437	GACACGGAGCGGCCGGTGAATCGGTTTCACTTGAAAAAGAAATGAGGGTCTGGCGGGAC	1180	1190	1200	1210	1220	1230
1247	GACACGGAGCGGCCGGTGAATCGGTTTCACTTGAAAAAGAAATGAGGGTCTGGCGGGAC	1510	1520	1530	1540	1550	1560
22437	TCCCTTCTTGGTGGAGAGGCAAGCTGCTACACAAAGAGACAAATGACAAAGTGGACGCC	1240	1250	1260	1270	1280	1290
1247	TCCCTTCTTGGTGGAGAGGCAAGCTGCTACACAAAGAGACAAATGACAAAGTGGACGCC	1570	1580	1590	1600	1610	1620
22437	CAGGAGGAGAACTTCTGCCCAAGTACCAGCGTGTGAAGGACCTGTGTCAAGCTGCTGAG	1300	1310	1320	1330	1340	1350
1247	CAGGAGGAGAACTTCTGCCCAAGTACCAGCGTGTGAAGGACCTGTGTCAAGCTGCTGAG	1630	1640	1650	1660	1670	1680

Fig. 3G

Fig. 3H

Fig. 31

SEQUENCE 22437

22437	1780	1790	1800	1810	1820	1830
	TACTCAGCCGCAACCCCATTAAGTGACACATCGGTGCTACATCCTAGAGAACGACACA					
1247	2110	2120	2130	2140	2150	2160
	TACTCAGCCGCAACCCCATTAAGTGACACATCGGTGCTACATCCTAGAGAACGACACA					
22437	1840	1850	1860	1870	1880	1890
	GTCCAGTGTGACCTGGACCTGTACAAGTCCCTGCAGGCCCTGGAAAAGACCACCAAGCTGCAC					
1247	2170	2180	2190	2200	2210	2220
	GTCCAGTGTGACCTGGACCTGTACAAGTCCCTGCAGGCCCTGGAAAAGACCACCAAGCTGCAC					
22437	1900	1910	1920	1930	1940	1950
	ATCGACCACGAGATTGAAACCCCTGCAGAACCAAAATTAAGAACCTGAGGGAAGTCCGAGGT					
1247	2230	2240	2250	2260	2270	2280
	ATCGACCACGAGATTGAAACCCCTGCAGAACCAAAATTAAGAACCTGAGGGAAGTCCGAGGT					
22437	1960	1970	1980	1990	2000	2010
	CACCTGAAGAAAAAGCGGCCAGAGAATGTGACTGTCACAAAAATCAGCTACCACACCCAG					
1247	2290	2300	2310	2320	2330	2340
	CACCTGAAGAAAAAGCGGCCAGAGAATGTGACTGTCACAAAAATCAGCTACCACACCCAG					

Fig. 3J

22437	2020	2030	2040	2050	2060	2070
	CACAAAGGCCGCCTCAAGCACAGAGCTCCAGTCTGCATCCTTTCAGGAAGGCCCTGCAA					
	::					
1247	CACAAAGGCCGCCTCAAGCACAGAGCTCCAGTCTGCATCCTTTCAGGAAGGCCCTGCAA					
	2350	2360	2370	2380	2390	2400
	2080	2090	2100	2110	2120	2130
22437	GAGAAAGGACAAAGGTGTGGCTGTTCGGGAGCAGAAGCGCAAGAAAGAACTCCGCAAGCTG					
	::					
1247	GAGAAAGGACAAAGGTGTGGCTGTTCGGGAGCAGAAGCGCAAGAAAGAACTCCGCAAGCTG					
	2410	2420	2430	2440	2450	2460
	2140	2150	2160	2170	2180	2190
22437	CTCAAGCGCCTGCAGAAACAACGACACGTGCAGCATGCCAGGCTTCACGTGCTTCACCCAC					
	::					
1247	CTCAAGCGCCTGCAGAAACAACGACACGTGCAGCATGCCAGGCTTCACGTGCTTCACCCAC					
	2470	2480	2490	2500	2510	2520
	2200	2210	2220	2230	2240	2250
22437	GACAAACGACACTGGCAGACGGCGCCTTCTGGACACTGGGCTTCTGTGCTGCACACC					
	::					
1247	GACAAACGACACTGGCAGACGGCGCCTTCTGGACACTGGGCTTCTGTGCTGCACACC					
	2530	2540	2550	2560	2570	2580

Fig. 3K

Sequence "A3366A"

22437	2260	2270	2280	2290	2300	2310
	AGGCCAACAAATAACACAGTACTGGTGCATGAGGACCATCAATGAGACTCACAATTTCCTC					
1247	2590	2600	2610	2620	2630	2640
	AGGCCAACAAATAACACAGTACTGGTGCATGAGGACCATCAATGAGACTCACAATTTCCTC					
22437	2320	2330	2340	2350	2360	2370
	TTCGTGAATTGCAACTGGCTTCCTAGAGTACTTTGATCTCAACACAGACCCCTACCAG					
1247	2650	2660	2670	2680	2690	2700
	TTCGTGAATTGCAACTGGCTTCCTAGAGTACTTTGATCTCAACACAGACCCCTACCAG					
22437	2380	2390	2400	2410	2420	2430
	CTGATGAATGCAGTGAACACACACTGGACAGGGATGTCTCAACCAGCTACACGTACAGCTC					
1247	2710	2720	2730	2740	2750	2760
	CTGATGAATGCAGTGAACACACACTGGACAGGGATGTCTCAACCAGCTACACGTACAGCTC					
22437	2440	2450	2460	2470	2480	2490
	ATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAACCCCGGACTCGAAACATGGAC					
1247	2770	2780	2790	2800	2810	2820
	ATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAACCCCGGACTCGAAACATGGAC					

Fig. 3L

```

2500      2510      2520      2530      2540      2550
CTGGGACTTAAAGATGGAGGAAGCTATGAGCAATACAGCAGTTTCAGCGTCGAAAGTGG
1247      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
CTGGGACTTAAAGATGGAGGAAGCTATGAGCAATACAGCAGTTTCAGCGTCGAAAGTGG
2830      2840      2850      2860      2870      2880

2560      2570      2580      2590      2600      2610
CCAGAAATGAAGAGACCTTCTTCCAAATCACTGGGACAACTGTGGGAAGGCTGGGAAGGT
22437      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
CCAGAAATGAAGAGACCTTCTTCCAAATCACTGGGACAACTGTGGGAAGGCTGGGAAGGT
2890      2900      2910      2920      2930      2940

TAA-----
1247      :::
TAAAGAAACAACAGAGGTTGGACCTCCAAAAACATAGAGGCATCACCTGACTGCACAGGCAA
2950      2960      2970      2980      2990      3000

-----

1247      TGAAAAACCATGTGGGTGATTTCCAGCAGACCTGTGCTATTGGCCAGGAGGCCTGAGAAA
3010      3020      3030      3040      3050      3060
```

Fig. 3M

22437 -----
1247 GCAAGCAGCACTCTCAGTCAACATGACAGATTCTGGAGGATAACCAGCAGGAGCAGAGA
3070 3080 3090 3100 3110 3120
22437 -----
1247 TAACTTCAGGAAGTCCATTTTTGCCCCCTGCTTTTGCTTTGGATTATACCTCACCCAGCTGC
3130 3140 3150 3160 3170 3180
22437 -----
1247 ACAAAATGCATTTTTCGTATCAAAAAGTCACCACCTAACCCCTCCCCCAGAAGCTCACAAA
3190 3200 3210 3220 3230 3240
22437 -----
1247 GGAAACGGAGAGCGGAGCGAGAGAGATTTCCTTGGAATTTCTCCCAAGGGCGAAAGT
3250 3260 3270 3280 3290 3300

Fig. 3N

Sequence

```
22437 -----  
1247 CATTGGAAATTTTAAATCATAGGGGAAAGCAGTCCTGTCTAAATCCTTATTCTTTT  
3310 3320 3330 3340 3350 3360  
22437 -----  
1247 GGTTCACAAAAGGAACCTAAGAAGCAGGACAGAGGCAACGTGGAGAGGCTGAAAAC  
3370 3380 3390 3400 3410 3420  
22437 -----  
1247 AGTGCAGAGACGTTTGACAAATGAGTCAGTAGCACAAAAGAGATGACATTTACCTAGCACT  
3430 3440 3450 3460 3470 3480  
22437 -----  
1247 ATAAACCCCTGGTTGCCCTCTGAAGAAACTGCCCTTCATTGTATATATGTGACTATTACATG  
3490 3500 3510 3520 3530 3540
```

Fig. 30

22437 -----
1247 TAATCAACATGGGAACCTTTAGGGGAACCTAATAAGAAATCCCAATTTTCAGGAGTGGTG
3550 3560 3570 3580 3590 3600
22437 -----
1247 GTGTCAATAAACGCTCTGTGGCCAGTGTAAGAAATCCCTCGCAGTTGTGGACATTTC
3610 3620 3630 3640 3650 3660
22437 -----
1247 TGTTCCTGTCCAGATAACCATTTCTCCTAGTATTTCTTGTATGTCCCAACTGATGTT
3670 3680 3690 3700 3710 3720
22437 -----
1247 TTTTTTTAAGGTACTGAAAAGAAATGAAGTTGATGATGTCCCAAGTTTGTATGAAACT
3730 3740 3750 3760 3770 3780

Fig. 3P

"GAGT" 232266

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22437 -----  
1247 GTATTGTAAAAAATTTGTAGTTTAAGTATTGTCATACAGTGTTCAAAACCCAGCC  
      3790      3800      3810      3820      3830      3840  
22437 -----  
1247 AATGACCAGCAGTTGGTATGAAGAACCTTTGACATTTTGTAAGGCCATTTCTTCTTG  
      3850      3860      3870      3880      3890      3900  
22437 -----  
1247 GGAGTTTTTGGTGTGTCGTGTTTTTTAAAGTATTCAAGATACTACCAGTCAACATCTTT  
      3910      3920      3930      3940      3950      3960  
22437 -----  
1247 TTGGAAGAAAATGCCCTTGGGTTTAGAAGATTTTCTTAAAGGGGAGTAGATGGTTGTAGA  
      3970      3980      3990      4000      4010      4020
```

Fig. 3Q

TABLE 22437

22437	-----	
1247	TTGACTAAAAAGTCTACCATACTTCAAGGGACTACAGGTAAGTCTCATAGTATACCAGCT	
	4030 4040 4050 4060 4070 4080	
22437	-----	
1247	TTGGTACTTCATTTTTTAAAAAGTATTAAATCAATTGCAAAGAAAATTCGCCTTGGCCCAAC	
	4090 4100 4110 4120 4130 4140	
22437	-----	
1247	CCTTCCTTGTGTATCAGGTAGTCTAACCTGATACAAAGTAGTTGACAGATTTCAACTATCA	
	4150 4160 4170 4180 4190 4200	
22437	-----	
1247	ATCACCAGTCCAACCCATTTCTCATTTAACAGATGACGGAGATAATCCCTAAAAGCACCC	
	4210 4220 4230 4240 4250 4260	

Fig. 3R

TEBAY 2222662

22437 -----
1247 ACATTTGTTTCAATGCCCCAAACAGGCCAAGGCTCCCTAGCAACTCCCTAGTGGCGTTT
4270 4280 4290 4300 4310 4320
22437 -----
1247 TTAACCTCTCAGAACTGTTACCATTTATTGAAATAGGCTTCCTTAACCTCCTTTACCCCT
4330 4340 4350 4360 4370 4380
22437 -----
1247 TAACCCAACAGGGATT
4390

Fig. 3S

22437	-----MGPPSLVCLLSATVFSLLGGSSAFLSHHRLKGRFQDRRNIRPN	10	20	30	40
1247	DSRIPEAPDQKKMGPPSLVCLLSATVFSLLGGSSAFLSHHRLKGRFQDRRNIRPN	10	20	30	40
22437	IILVLTDDQDVELGSMQVMNKTRRIMEQGGTHFINAFVTTMCCPSRSSILTGKYVHNHN	50	60	70	80
1247	IILVLTDDQDVELGSMQVMNKTRRIMEQGGTHFINAFVTTMCCPSRSSILTGKYVHNHN	70	80	90	100
22437	TYTNNENCSSPSWQAQHEsrTFaVYLNstGYrTAFfGKYlNEYNGSYVPPGWKEWVGLLK	110	120	130	140
1247	TYTNNENCSSPSWQAQHEsrTFaVYLNstGYrTAFfGKYlNEYNGSYVPPGWKEWVGLLK	130	140	150	160
22437	NSRFYNYTLCRNGVKEKHGSDYskDyLTdLiTNDSVsfFRTskKMyPhRPVLMVISHAAP	170	180	190	200
1247	NSRFYNYTLCRNGVKEKHGSDYskDyLTdLiTNDSVsfFRTskKMyPhRPVLMVISHAAP	190	200	210	220

Fig. 4A

SEQUENCE

230	240	250	260	270	280
22437	HGPEDSAPQYSRLFPNASQHI	TPSYNAPNPDKHWIMRYTGPMKPI	HMEFTNMLQ	RKRLQ	
	::::::::::::::::::::::::	::::::::::::::::::::::::	::::::::::::::::	::::::::	
1247	HGPEDSAPQYSRLFPNASQHI	TPSYNAPNPDKHWIMRYTGPMKPI	HMEFTNMLQ	RKRLQ	
	250	260	270	280	300
22437	290	300	310	320	330
	TLMSVDDSMETIYNMLVETGEL	DNTYIVYTADHGYHIGQFGL	VKGKSM	PYEFDIRVPFYV	
	::::::::::::::::::::::::	::::::::::::::::	::::::::	::::::::	
1247	TLMSVDDSMETIYNMLVETGEL	DNTYIVYTADHGYHIGQFGL	VKGKSM	PYEFDIRVPFYV	
	310	320	330	340	360
22437	350	360	370	380	390
	RGPNVEAGCLNPHIVLNIDLA	PTILDIAGLDIPADMDGKSIL	KLDDTERP	VNRFHLKKM	
	::::::::::::::::::::::::	::::::::::::::::	::::::::	::::::::	
1247	RGPNVEAGCLNPHIVLNIDLA	PTILDIAGLDIPADMDGKSIL	KLDDTERP	VNRFHLKKM	
	370	380	390	400	420
22437	410	420	430	440	450
	RVWRDSFLVERGKLLHKRD	NKVDQAQEEENFLPKYQ	RVKDL	CQRAEYQ	TACEQLGQKWQCV
	::::::::::::::::::::::::	::::::::::::::::	::::::::	::::::::	
1247	RVWRDSFLVERGKLLHKRD	NKVDQAQEEENFLPKYQ	RVKDL	CQRAEYQ	TACEQLGQKWQCV
	430	440	450	460	480

Fig. 4B

22437 1247

22437	470	480	490	500	510	520
	EDATGK	KLHKCK	GPMRLG	SRALSN	LVPKYY	QGSEACTC
	DSGDYK	LSLAGR	RKKLFKK			
1247						
	EDATGK	KLHKCK	GPMRLG	SRALSN	LVPKYY	QGSEACTC
	DSGDYK	LSLAGR	RKKLFKK			
	490	500	510	520	530	540
22437	530	540	550	560	570	580
	KYKASY	VRSR	SIRSV	AEVDGR	VYHVGL	GDAAQPR
	NLTKR	HWPG	APEDQ	DDKDG	DFS	SGT
1247						
	KYKASY	VRSR	SIRSV	AEVDGR	VYHVGL	GDAAQPR
	NLTKR	HWPG	APEDQ	DDKDG	DFS	SGT
	550	560	570	580	590	600
22437	590	600	610	620	630	640
	GGLPDY	SAAN	PIKV	THRCYI	LENDTV	QC
	LDLYK	SLQAW	KDHL	HIDHEI	ETLQ	NKIKNL
1247						
	GGLPDY	SAAN	PIKV	THRCYI	LENDTV	QC
	LDLYK	SLQAW	KDHL	HIDHEI	ETLQ	NKIKNL
	610	620	630	640	650	660
22437	650	660	670	680	690	700
	REVRGH	LKKR	PEEC	CHKIS	YHTQ	HKGR
	LGSS	LHPFR	KGLQ	EKDK	VWLL	REQR
1247						
	REVRGH	LKKR	PEEC	CHKIS	YHTQ	HKGR
	LGSS	LHPFR	KGLQ	EKDK	VWLL	REQR
	670	680	690	700	710	720

Fig. 4C

Sequence

22437	710	720	730	740	750	760	
	KLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLGPFCACTSANNNTYWCMRTINE						
1247	730	740	750	760	770	780	
	THNLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQLHVQLMELRSCKGYKQCNP						
22437	770	780	790	800	810	820	
	TRNMDLGLKDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG						
1247	790	800	810	820	830	840	
	TRNMDLGLKDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG						
22437	830	840	850	860	870		
	TRNMDLGLKDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG						
1247	850	860	870	880			

Fig. 4D